

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bednarik, Daniel P.
Olsen, Henrik S.
Rosen, Craig A.
- (ii) TITLE OF INVENTION: Soluble Interleukin-1 Receptor Accessory
Molecule
- (iii) NUMBER OF SEQUENCES: 30
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVE., N.W., SUITE 600
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/024,581
 - (B) FILING DATE: 26-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Steffe, Eric K.
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.0450001/EKS/KMT
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 303..1370

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 303..353

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 354..1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGTGGCGCC CGTTCTAGAA CTAGTGGATC CCCCAGGATG CAGGAATTCG GCACGAGAAA	60
GTGCGGCGGA AAGTAAGAGG CTCACTGGGG AAGACTGCCG GGATCCAGGT CTCCGGGGTC	120
CGCTTTGGCC AGAGGCGCGG AAGGAAGCAG TGCCCGGCGA CACTGCACCC ATCCCGGCTG	180
CTTTTGCTGC GCCCTCTCAG CTTCCCAAGA AAGGCATCGT CATGTGATCA TCACCTAAGA	240
ACTAGAACAT CAGCAGGCCC TTAGAAGCCT CACTCTTGCC CCTCCCTTTA ATATCTCAAA	300
GG ATG ACA CTT CTG TGG TGT GTA GTG AGT CTC TAC TTT TAT GGA ATC	347
Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile	
-17 -15 -10 -5	
CTG CAA AGT GAT GCC TCA GAA CGC TGC GAT GAC TGG GGA CTA GAC ACC	395
Leu Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr	
1 5 10	
ATG AGG CAA ATC CAA GTG TTT GAA GAT GAG CCA GCT CGC ATC AAG TGC	443
Met Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys	
15 20 25 30	
CCA CTC TTT GAA CAC TTC TTG AAA TTC AAC TAC AGC ACA GCC CAT TCA	491
Pro Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser	
35 40 45	
GCT GGC CTT ACT CTG ATC TGG TAT TGG ACT AAG CAG GAC CGG GAC CTT	539
Ala Gly Leu Thr Leu Ile Trp Tyr Trp Thr Lys Gln Asp Arg Asp Leu	
50 55 60	
GAG GAG CCA ATT AAC TTC CGC CTC CCC GAG AAC CGC ATT AGT AAG GAG	587
Glu Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu	
65 70 75	
AAA GAT GTG CTG TGG TTC CGG CCC ACT CTC CTC AAT GAC ACT GGC AAC	635
Lys Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn	
80 85 90	
TAT ACC TGC ATG TTA AGG AAC ACT ACA TAT TGC AGC AAA GTT GCA TTT	683

Tyr	Thr	Cys	Met	Leu	Arg	Asn	Thr	Thr	Tyr	Cys	Ser	Lys	Val	Ala	Phe		
95					100					105					110		
CCC	TTG	GAA	GTT	GTT	CAA	AAA	GAC	AGC	TGT	TTC	AAT	TCC	CCC	ATG	AAA	731	
Pro	Leu	Glu	Val	Val	Gln	Lys	Asp	Ser	Cys	Phe	Asn	Ser	Pro	Met	Lys		
				115					120					125			
CTC	CCA	GTG	CAT	AAA	CTG	TAT	ATA	GAA	TAT	GGC	ATT	CAG	AGG	ATC	ACT	779	
Leu	Pro	Val	His	Lys	Leu	Tyr	Ile	Glu	Tyr	Gly	Ile	Gln	Arg	Ile	Thr		
				130				135					140				
TGT	CCA	AAT	GTA	GAT	GGA	TAT	TTT	CCT	TCC	AGT	GTC	AAA	CCG	ACT	ATC	827	
Cys	Pro	Asn	Val	Asp	Gly	Tyr	Phe	Pro	Ser	Ser	Val	Lys	Pro	Thr	Ile		
		145					150					155					
ACT	TGG	TAT	ATG	GGC	TGT	TAT	AAA	ATA	CAG	AAT	TTT	AAT	AAT	GTA	ATA	875	
Thr	Trp	Tyr	Met	Gly	Cys	Tyr	Lys	Ile	Gln	Asn	Phe	Asn	Asn	Val	Ile		
	160					165					170						
CCC	GAA	GGT	ATG	AAC	TTG	AGT	TTC	CTC	ATT	GCC	TTA	ATT	TCA	AAT	AAT	923	
Pro	Glu	Gly	Met	Asn	Leu	Ser	Phe	Leu	Ile	Ala	Leu	Ile	Ser	Asn	Asn		
175				180						185					190		
GGA	AAT	TAC	ACA	TGT	GTT	GTT	ACA	TAT	CCA	GAA	AAT	GGA	CGT	ACG	TTT	971	
Gly	Asn	Tyr	Thr	Cys	Val	Val	Thr	Tyr	Pro	Glu	Asn	Gly	Arg	Thr	Phe		
				195					200					205			
CAT	CTC	ACC	AGG	ACT	CTG	ACT	GTA	AAG	GTA	GTA	GGC	TCT	CCA	AAA	AAT	1019	
His	Leu	Thr	Arg	Thr	Leu	Thr	Val	Lys	Val	Val	Gly	Ser	Pro	Lys	Asn		
			210					215					220				
GCA	GTG	CCC	CCT	GTG	ATC	CAT	TCA	CCT	AAT	GAT	CAT	GTG	GTC	TAT	GAG	1067	
Ala	Val	Pro	Pro	Val	Ile	His	Ser	Pro	Asn	Asp	His	Val	Val	Tyr	Glu		
		225						230				235					
AAA	GAA	CCA	GGA	GAG	GAG	CTA	CTC	ATT	CCC	TGT	ACG	GTC	TAT	TTT	AGT	1115	
Lys	Glu	Pro	Gly	Glu	Glu	Leu	Leu	Ile	Pro	Cys	Thr	Val	Tyr	Phe	Ser		
	240					245					250						
TTT	CTG	ATG	GAT	TCT	CGC	AAT	GAG	GTT	TGG	TGG	ACC	ATT	GAT	GGA	AAA	1163	
Phe	Leu	Met	Asp	Ser	Arg	Asn	Glu	Val	Trp	Trp	Thr	Ile	Asp	Gly	Lys		
255					260				265					270			
AAA	CCT	GAT	GAC	ATC	ACT	ATT	GAT	GTC	ACC	ATT	AAC	GAA	AGT	ATA	AGT	1211	
Lys	Pro	Asp	Asp	Ile	Thr	Ile	Asp	Val	Thr	Ile	Asn	Glu	Ser	Ile	Ser		
				275				280					285				
CAT	AGT	AGA	ACA	GAA	GAT	GAA	ACT	AGA	ACT	CAG	ATT	TTG	AGC	ATC	AAG	1259	
His	Ser	Arg	Thr	Glu	Asp	Glu	Thr	Arg	Thr	Gln	Ile	Leu	Ser	Ile	Lys		
			290					295				300					
AAA	GTT	ACC	TCT	GAG	GAT	CTC	AAG	CGC	AGC	TAT	GTC	TGT	CAT	GCT	AGA	1307	
Lys	Val	Thr	Ser	Glu	Asp	Leu	Lys	Arg	Ser	Tyr	Val	Cys	His	Ala	Arg		
		305					310					315					

AGT GCC AAA GGC GAA GTT GCC AAA GCA GCC AAG GTG AAG CAG AAA GGT	1355
Ser Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Gly	
320 325 330	
 AAT AGA TGC GGT CAG TGATGAATCT CTCAGCTCCA AATTAACATT GTGGTGAATA	1410
Asn Arg Cys Gly Gln	
335	
 AGGACAAAAG GAGAGATTGA GAACAAGAGA GCTCCAGCAC CTAGCCTGAC GGCATCTAAC	1470
CCATAGTAAT GAATCAAAC TAAATGAAAA ATATGAAAGT TTTCATCTAT GTAAGATACT	1530
CAAAATATTG TTTCTGATAT TGTTAGTACC GTAATGCCCA AATGTAGCTA AAAAAATCGA	1590
CGTGAGTACA GTGAGACACA ATTTTGTGTC TGTACAATTA TGAAAAATTA AAAACAAAGA	1650
AAATATTCAA AGCTACCAAA GATAGAAAAA ACTGGTAGAG CCACATATTG TTGGTGAATT	1710
ATTAAGACCC TTTTAAAAAT CATTTCATGGT AGAGTTTAAAG AGTCATAAAA AAGATTGCAT	1770
CATCTGACCT AAGACTTTTCG GAATTTTTTCC TGAACAAATA ACAGAAAGGG AATTATATAC	1830
CTTTTAATAT TATTAGAAGC ATTATCTGTA GTTGTAATAAC ATTATTAATA GCAGCCATCC	1890
AATTGTATGC AACTAATTAA GGTATTGAAT GTTTATTTTC CAAAAATGCA TAATTATAAT	1950
ATTATTTTAA ACACTATGTA TCAATATTTA AGCAGGTTTA TAATATACCA GCAGCCACAA	2010
TTGCTAAAAT GAAAATCATT TAAATTATGA TTTTAAATGG TATACACATG ATTTCTATGT	2070
TGATAGTACT ATATTATTCT ACAATAAATG GAAATTATAA AGCCTTCTTG TCAGAAGTGC	2130
TGCTCCTAAA AAAAAAAAAA AAAAA	2155

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu	
-17 -15 -10 -5	
 Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met	
1 5 10 15	
 Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro	
20 25 30	

Leu	Phe	Glu	His	Phe	Leu	Lys	Phe	Asn	Tyr	Ser	Thr	Ala	His	Ser	Ala	
			35					40					45			
Gly	Leu	Thr	Leu	Ile	Trp	Tyr	Trp	Thr	Lys	Gln	Asp	Arg	Asp	Leu	Glu	
		50					55					60				
Glu	Pro	Ile	Asn	Phe	Arg	Leu	Pro	Glu	Asn	Arg	Ile	Ser	Lys	Glu	Lys	
	65					70				75						
Asp	Val	Leu	Trp	Phe	Arg	Pro	Thr	Leu	Leu	Asn	Asp	Thr	Gly	Asn	Tyr	
80					85					90					95	
Thr	Cys	Met	Leu	Arg	Asn	Thr	Thr	Tyr	Cys	Ser	Lys	Val	Ala	Phe	Pro	
				100					105					110		
Leu	Glu	Val	Val	Gln	Lys	Asp	Ser	Cys	Phe	Asn	Ser	Pro	Met	Lys	Leu	
			115					120					125			
Pro	Val	His	Lys	Leu	Tyr	Ile	Glu	Tyr	Gly	Ile	Gln	Arg	Ile	Thr	Cys	
	130						135					140				
Pro	Asn	Val	Asp	Gly	Tyr	Phe	Pro	Ser	Ser	Val	Lys	Pro	Thr	Ile	Thr	
	145					150					155					
Trp	Tyr	Met	Gly	Cys	Tyr	Lys	Ile	Gln	Asn	Phe	Asn	Asn	Val	Ile	Pro	
160					165					170					175	
Glu	Gly	Met	Asn	Leu	Ser	Phe	Leu	Ile	Ala	Leu	Ile	Ser	Asn	Asn	Gly	
			180						185					190		
Asn	Tyr	Thr	Cys	Val	Val	Thr	Tyr	Pro	Glu	Asn	Gly	Arg	Thr	Phe	His	
			195					200					205			
Leu	Thr	Arg	Thr	Leu	Thr	Val	Lys	Val	Val	Gly	Ser	Pro	Lys	Asn	Ala	
		210					215					220				
Val	Pro	Pro	Val	Ile	His	Ser	Pro	Asn	Asp	His	Val	Val	Tyr	Glu	Lys	
	225					230					235					
Glu	Pro	Gly	Glu	Glu	Leu	Leu	Ile	Pro	Cys	Thr	Val	Tyr	Phe	Ser	Phe	
240					245					250					255	
Leu	Met	Asp	Ser	Arg	Asn	Glu	Val	Trp	Trp	Thr	Ile	Asp	Gly	Lys	Lys	
				260					265					270		
Pro	Asp	Asp	Ile	Thr	Ile	Asp	Val	Thr	Ile	Asn	Glu	Ser	Ile	Ser	His	
			275					280					285			
Ser	Arg	Thr	Glu	Asp	Glu	Thr	Arg	Thr	Gln	Ile	Leu	Ser	Ile	Lys	Lys	
		290					295					300				
Val	Thr	Ser	Glu	Asp	Leu	Lys	Arg	Ser	Tyr	Val	Cys	His	Ala	Arg	Ser	
	305					310					315					
Ala	Lys	Gly	Glu	Val	Ala	Lys	Ala	Ala	Lys	Val	Lys	Gln	Lys	Gly	Asn	

320

325

330

335

Arg Cys Gly Gln

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Leu	Leu	Trp	Tyr	Leu	Met	Ser	Leu	Ser	Phe	Tyr	Gly	Ile	Leu	1	5	10	15
Gln	Ser	His	Ala	Ser	Glu	Arg	Cys	Asp	Asp	Trp	Gly	Leu	Asp	Thr	Met	20	25	30	
Arg	Gln	Ile	Gln	Val	Phe	Glu	Asp	Glu	Pro	Ala	Arg	Ile	Lys	Cys	Pro	35	40	45	
Leu	Phe	Glu	His	Phe	Leu	Lys	Tyr	Asn	Tyr	Ser	Thr	Ala	His	Ser	Ser	50	55	60	
Gly	Leu	Thr	Leu	Ile	Trp	Tyr	Trp	Thr	Arg	Gln	Asp	Arg	Asp	Leu	Glu	65	70	75	80
Glu	Pro	Ile	Asn	Phe	Arg	Leu	Pro	Glu	Asn	Arg	Ile	Ser	Lys	Glu	Lys	85	90	95	
Asp	Val	Leu	Trp	Phe	Arg	Pro	Thr	Leu	Leu	Asn	Asp	Thr	Gly	Asn	Tyr	100	105	110	
Thr	Cys	Met	Leu	Arg	Asn	Thr	Thr	Tyr	Cys	Ser	Lys	Val	Ala	Phe	Pro	115	120	125	
Leu	Glu	Val	Val	Gln	Lys	Asp	Ser	Cys	Phe	Asn	Ser	Ala	Met	Arg	Phe	130	135	140	
Pro	Val	His	Lys	Met	Tyr	Ile	Glu	His	Gly	Ile	His	Lys	Ile	Thr	Cys	145	150	155	160
Pro	Asn	Val	Asp	Gly	Tyr	Phe	Pro	Ser	Ser	Val	Lys	Pro	Ser	Val	Thr	165	170	175	
Trp	Tyr	Lys	Gly	Cys	Thr	Glu	Ile	Val	Asp	Phe	His	Asn	Val	Leu	Pro	180	185	190	

Glu Gly Met Asn Leu Ser Phe Phe Ile Pro Leu Val Ser Asn Asn Gly	
195	200 205
Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Leu Phe His	
210	215 220
Leu Thr Arg Thr Val Thr Val Lys Val Val Gly Ser Pro Lys Asp Ala	
225	230 235 240
Leu Pro Pro Gln Ile Tyr Ser Pro Asn Asp Arg Val Val Tyr Glu Lys	
	245 250 255
Glu Pro Gly Glu Glu Leu Val Ile Pro Cys Lys Val Tyr Phe Ser Phe	
	260 265 270
Ile Met Asp Ser His Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys	
	275 280 285
Pro Asp Asp Val Thr Val Asp Ile Thr Ile Asn Glu Ser Val Ser Tyr	
	290 295 300
Ser Ser Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys	
305	310 315 320
Val Thr Pro Glu Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn	
	325 330 335
Thr Lys Gly Glu Ala Glu Gln Ala Ala Lys Val Lys Gln Lys	
	340 345 350

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTATGAGAA AGAACAAGGA GAGGAGCTAC TCATTCCCTG TACGGTCTAT TTTAGTTTTT	60
TGATGGATTC TCGCAATGAG GTTTGGTGGA CCATTGATGG AAAAAACCT GATGACATCA	120
CTATTGATGT CACCATTAAAC GAAAGTATAA GTCATAGTAG AACAGAAGAT GAAACAAGAA	180
CTCAGATTTT GAGCATCAAG AAAGTTACCT CTGAGGATCT CAAGCGCANT ANTGTCTGTC	240
ATGCTAGAAG TGCCAAAGGC GAAGTTGCCA AAGCAGCCAA GGTGAAGCAG AAAG	294

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGAACCTCC AACATATAG AAGTAAAGAC ACAGGGCTGT TATAAAATAC AGAATTTTAA	60
TAATGTAATA CCCGAAGGTA TGANCTTGAG TTCCTCATT GCCTTAATTT CAAATAATGG	120
AAATTACACA TGTNTTGTTA CATATCCAGA AAATGGACGT ACGTTTCATC TCACCAGGAC	180
TCTGCTCTNT AAAGGTAGTA GGCTCTCCAA AAANTGCAGT GCCCCCTGTG ATCCATTCAC	240
CTAATGATCA TG	252

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGACAGCGT CTTGCTCTGT CACCTGGGCT GGAGTGCAGT GGCGAGATCT CGGCTCACTG	60
CAACCTCTGC CTCCCAGGTT CAAGCAATTC TCCTGCCTCA CCCTCCTGAG TAGCTGGGAT	120
TACAGGTGTA TGCCACCATG CCGGCTAATT TTTGTATTTT CTAGTAGAGA CTAGGTTTCA	180
CCATGTTGGC CAGGCTGGTC TTGAACTATT TTTTTTCTT TTTCTCGTGC CGAATTCCTG	240
CAGCCCGGGG GATCCACTAG TTCTAGAGCG GCCGCCACCG CGGTGGAGCT CCAGCTTTTG	300
TTCCCTTTAG TGAGGGNTAA TTTCGAGCTT GCGGTAATCA TGGTCATAGC TGTTTCCTGT	360
GTGAAATTGT TATCCGCTCA CAATTTTACA CAACATACGA GCCGGAAGCA TAAAGTGTA	420

AGCCT

425

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCACNNAAGG GACAAAAGCT GGAGCTCCAC CGCGGGCNGC NCGTTCTAGA ACTAGTGGAT	60
CCCCCGGGCT GCAGGAATTC	80

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAACTAGTGG ATCCCCCGGG CTGCAGGAAT TCGNCACGAG ACCANCTCAC CTTTCCCCAC	60
ACTAGCTCAN GNACAGACAG ANTGGACTAA AAATAGTTGA	100

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GNCTAGAACT AGTGGATCCC CCGGGCTGCA GGAATTCGGC ACGAGGGGCT GCTCGAGCTG	60
CCAACAACGG AGCATTGCCC CCTGGACCTN AGCTGACATC GTGCGTAGNC TAGGCATGNG	120
TGGTTGTAGG GACTTACGTC TTTCTACNT GANNCACGGT TATCACTGNC GANGTCCACC	180
CACCGGGGNT GNNCAACTTN CGGNGGAAGG TACTACNTAC TTCAAACCC CCTAACTTGT	240
TCCTTTTTTG CAGGATCGAG TN	262

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

NTTAGTGTAC AGACACAAAA TTGTGTCTCA CTGTACTCAC GTCGATTTTT TTAGCTACAT	60
TTGGGCATTA CGGTACTAAC AATATCAGAA ACAATATTTT GAGTATCTTA CATAGATGAA	120
AACTTTCATA TTTTTCATTT AAGTTTGATT CATTACTATG GGTTAGATGC CGTCGGNTAG	180
GTGCTGGAGC TCTCTGTTC TCAATCTCTC CTTTTGTCCT TATTCACCAC AATGTTAATT	240
TGGAGCTGAG AGATTCACTA CTGACCGCAT CTATTACCTT TCTGCTTCAC CTTGGCTGCT	300
TTGGCAACTT CGCCTTTGGA CCTTCTAGCA TGACAGACAT AGCTGCGCTT GAGATCCTCA	360
GAGGTAAGTT TCTTGANGCT CAAAATCTGA GTTCTTGTTT C	401

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATAATTGTA CAGACACAAA ATTGTGTCTC ACTGTACTCA CGTCGATTTT TTAGCTACA	60
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TTTGGGCATT ACGGTACTAA CAATATCAGA AACAAATATTT TGAGTATCTT ACATAGATGA	120
AAACTTTCAT ATTTTTCATT TAAGTTTNGA TTCATTACTA TGGGTTAGAT GCCGTCGGGC	180
TNAGGTGCTG GAGCTCTCTT GTTCTCAATC TCTCCTTTTG TCCTTATTCA CCACAATGTT	240
AATTTGGAGC TGAGAGATTC ATCACTGACC GCATCTATTA CCTTTCTGCT TCACCTTGGC	300
TCGCTTTGGC AACTTCGCCT TTGGACTTCT AGCATGACAG ACATAGCTGC GCTTGGAGAT	360
CCTCAGAGGT AACTTTCCTG ATGGCTCAAA ATCNGAGTTC TTGTTTCATC TTCTGTTCTA	420
CTATGACTTA TACTTTCGTT AAN	443

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CATAATTGTA CAGACACAAA ATTGTGCTCA CTGTACNCAC GTCGATTTTT TTAGCTACAT	60
TTGGGCATTA CGGTACTAAC AATATCAGAA ACAATATTTT GAGTATCTTA CATAGATGAA	120
AACTTTCATA TTTTTCATTT AAGTTTGATT CATTACTATG GGTTAGATGC CGTCGGGCTA	180
GGGGCTGGAG CTCTCTTGTT CTCAATCTCT CCTTTTGTCC TTATTCACCA CAATGTTAAT	240
TTGGNGCTGA GAGATTCATC ACTGACCGCA TCTATTACCN TTCTGCTTCA NCTTGGCTGC	300
TTTGGNAACT TCGNCTTTG	319

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCTATGAGAA AGAACCAGGA GAGGAGCTAC TCATTCCCTG TACGGTCTAT TTTAGTTTTC	60
TGATGGATTC TCGCAATGAG GTTTGGTGGG CCATTGATGG AAAAAACCT GATGACATCA	120
CTATTGATGT CACCATTAAC GAAAGTATAA GTCATAGTAG AACAGAAGAT GAAACAAGAA	180
CTCAGATTTT GAGCATCAAG AAAGTTACCT CTGAGGATCT CAAGCGCANT ANTGTCTGTC	240
ATGCTAGAAG TGCCAAAGGC GAAGTTGCCA AAGCAGCCAA GGTGAAGCAG AAAGTGCCAG	300
CTCCAAGATA CACAGTGGAA CTGGCTTGTC GTTTTGGAGC CACAGTCCTG CTAGTGGTGA	360
TTCTCATTGT TGTTTACCAT GTTTACTTGG CTAGAG	396

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTCTCCAAA AAATGCAGTG CCCCTGTGA TCCATTCAAC TAATGATCAT GTGGTCTATG	60
AGAAAGAACC AGGAGAGGAG CTACTCATTC CCTGTACGGT CTATTTTAGT TTTCTGATGG	120
ATTCTCGCAA TGAGGTTTGG TGGACCATTG ATGGAAAAAA ACCTGATGAC ATCACTATTG	180
ATGTCACCAT TAACGAAAGT ATAAGTCATA GTAGAACAGA AGATGAAACA AGAACTCAGA	240
TTTTGAGGCA TCAAGAAAGT TACCTCTGAG GATCTCAAGC GCNTAATNGT CTGTNCATGG	300
CTAGGAAGTG CCAAAGNGGA AGTTGGCCAA AGGCAGCCAA GGTNGAGGCA GGAAAGGTTA	360
TTAGGTGGCG GTTCAGTTGA TGGATTCTCT TCAGGNTCCC AATTTTAACN TTGTTGGGTG	420
GATTTA	426

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 570 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCGGCACAG GGAACCTCCA AACATATAGA AGTAAAGACA CAGGGCTGTT ATAAAATACA	60
GAATTTTAAT AATGTAATAC CCGAAGTATG AACTTGAGTT TCCTCATTGC CTTAATTTCA	120
AATAATGGAA ATTACACATG TGTGTTTACA TATCCAGAAA ATGGACGTAC GTTTCATCTC	180
ACCAGGACTC TGA CTGTAAA GGTAGTAGGC TCTCCAAAAA ATGCAGTGCC CCCTGTGATC	240
CATTACCTA ATGATCATGT GGTCTATGAG AAAGAACCAG GGAGAGTAGC TACTCATTCC	300
CTGTACGGTC TATTTTAGTT TTCTGATGGA TTCTCGCAAT GGAGGTTTNG TGGGACCATT	360
TGATGGGAAA AAAACCTGGA TNGACATCAN TATTTGATGT TCACCATTTA ACGGAAAGTA	420
TTAAGTCCTT AGTTAGGANC AGGTGGTTGA ANACAGGAAN TCCGGTTTTT GAGGCTTCAG	480
GAAAGTTTAC CCCTGNGGGT TCTTCAGGNG CCGATTGTTN TGTCNTTGT TNGGAGGTGN	540
CCCAGNGGAA GTTTTGNCCA AGGCGGCCAG	570

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAGTACTATC AACATAGAAA NCATGTTTAT ACCATTTAAA ATCATAATTT AAATGATTTT	60
CATTTTAGCA ATTGTGGCTG CTGGTATATT ATAAACCTGC TTAAATATTG ATACATAGTG	120
TTTAANATAA TATTATAATT CTGCATTTTT GGAAAATAAA CATTCAATAC CTTAATTAGT	180
TGCATACAAT TGGATGGCTG CTATTAATAA NGTTTACAA CTACAGATAA TGCTTCTAAT	240
ANTATTANCG GGNATA	256

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAACAGAAGA TGAAACAAGA ACTCAGATTT TGAGCATCAA GAAAGTTACC TCTGAGGATC	60
TCAAGCGCAN TATTGTCTGT CATGCTAGAA GTGCCAAAGG GAANGTTGCC AAAGCAGCCA	120
AGGTGAAGCA GAAAGGTAAT AGATGCGGTC AGTGATGAAT CTCTCAGCTC CAAATTAACA	180
TTGTGGGTGA ATAAGGACAA AAGGAGAGAT TGAGGAACAA GAGAGCTCCA GCACCTAGCC	240
TGACGGCATC TTAACCCCAT AGTAATTGAA TCCAACTTTA AATGGAAAAN TTTGNAGTTT	300
TTTCATCCTT NGGTAGGGTA CTTCAANTTT TGT	333

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCTGACAAG AAGGCTTTAT AATTTCCATT TATTGTAGAA TAATATAGTA CTATCAACAT	60
AGAAATCATG TGTATACCAT TAAAATCAT AATTTAAATG ATTTTCATTT TAGCAATTGT	120
GGCTGCTGGG ATATTATAAA CTGCTTAAA TATTGATACA TAGNGTTTAA AATAATATTA	180
TAATTATGCA NTTTTGGGGA AATAAACATT CAATACCCNT AATAGGTGCA TACAATTGGG	240
AGGGCTGCNA TTAATAATGG TTTCCACNAC C	271

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TATTTTCCAA AAATGCATAA TTATAATATT ATTTYAMMCA CTATGTATCA ATATTTAAGC	60
AGGTTTATAA TATACCAGCA GCCACAATTG CTAAAATGAA AATCATTAA ATTATGATTT	120
TAAATGGTAT ACACATGATT YCTATGTTGA TAGTACTATA TTATTCTACA ATAAATGGAA	180
ATTATAACGC CTTCTTGTCA GAAGTGCTGC TCCT	214

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCTTTATAAT ATTTTANTTA TTGTAGAATA ATATAGTACT ATCAACATAG AAATCATGTG	60
TATACCATTT AAAATCATAA TTTAAATGAT TTTCAATTTTA GCAATTGTGG CTGCTGGGTA	120
TATTATAAAC CTGCTTAAAT ATTGATACAT AGTGTTTAAA ATAATATTAT AATTATGGCA	180
TTTTTGGGAA ATAAACATTC AATACCTTAA TTGGNTGGCA TACAATGGGG TGGGCNGGCT	240
ATTAATAATG GTTTTACAAC TACAGGGTAA TGGCNTCCTA ATAATATTAA AGGGGGGNTA	300
TAATTCCTCC	309

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGGNGTCCG CTTTGGCCAG ANGTINGGAAG GAAGCAGTGC CCGGCGACAC TCCACCCATC	60
CCGGCTGCTT TTGCTGCGCC CTCTCAGCTT CCCAAGAAAG GATGACACTT CTGTGGTGTG	120
TAGTGAGTCT CTACTTTTAT GGAATCCTGC AAAGTGATGC CTCAGGTAAG TGAATGGCTT	180
TTGACAATGT ATTAAAATGC AAGTCATGCG TAGGGTAATG AGTCCACTCT TCCTGAAAAT	240
GAATTTAAAT AACATAATG TTATTCATGT CCATTGTCTT CTGCGGTANA ANATNAATCA	300
TAAAGCAGAA TAATAGAATT TTGATGATGG GAAAGAACCA TTGCTGTCTC TAGTCTTCAT	360
GGGGATAGGA GTACACAGGG GGCAGTGGGG CCGCTGTGTT TTAAACACAG GTATTTTTC	420
NTACCTTCAC ATTACAGCAA CTAGGATATT TGCTTTTTTC CTTACCTCAG TCCCTTGGGG	480
GAAAAAT	486

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TAATGATCAT GTGGTCTATG AGAAAGAACC AGGANAGGAG CTACTCATTC CCTGTACGGT	60
TATTTTAGTT TTCTGATGGA TTCTCGCAAT GAGGTTTGGT GGACCATTGA TGGANAAAAA	120
CCTGATGACA TCACTATTNG ATTGTCAACA TTAAACNGA	159

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCCATGA CACTTCTGTG GTGTG	25
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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCGACTCAC TGACCGCATC T

21

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGATCCATCC GCCATCATGA CACTTCTGTG GTGTG

35

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCTAGAAAAG CGTAGTCTGG GACGTCGTAT GGGTACTGAC CGCATCT

47

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACTGGATCC GCCATCATGA CACTTCTGTG GTGTG

35

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCCTCA CTGACCGCAT CT

22

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GACTGGATCC GCCATCATGA CACTTCTGTG GTGTG

35

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GACTGGTACC CATAGAAATC ATGTGTATAC C

31